6-Paleoploidization events in the *Musa* (banana) lineage

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Bananas (*Musa* spp.) are giant perennial monocotyledonous herbs of the order Zingiberales, a sister group to the well-studied Poales. Cultivars are mainly triploid, from inter(sub)specific origin and clonally propagated. We sequenced the genome of a *Musa acuminata* doubled-haploid genotype (Pahang-HD) providing the first monocotyledon high-continuity whole-genome sequence reported outside Poales. The analysis of the genome revealed three rounds of whole genome duplications (WGD), denoted as alpha, beta and gamma (from the most recent event to the oldest). Based on Ks analyses and synteny relationships, twelve beta *Musa* ancestral blocks were constructed, representing the ancestral genome before alpha and beta duplications. Comparative genomics and phylogenetic approaches revealed that these three WGDs occurred in the *Musa* lineage independently of those described in the Poales lineage and the one that we detected in the Arecales lineage. Following WGDs, that are particularly frequent in the flowering plant lineages, most duplicated genes are deleted by intrachromosomal recombination, a process referred to as fractionation. We are currently analyzing the fractionation pattern following the *Musa* polyploidization events. Finally, this *Musa* reference sequence represents an invaluable reference for studying monocot evolution and associated genomic changes.